

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 09:57:31 ; Search time 2016.58 Seconds
(without alignments)
3628.854 Million cell updates/sec

Title: US-09-602-833a-3
Perfect score: 681
Sequence: 1 atggaattcgcgactcgcgc.....ctttagccttcaatttga 681

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_hic:*
10: gb_est1:*
11: gb_est2:*
12: gb_hic:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rnd:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	493.8	72.5	1450	12	AK010252 Mus muscu
2	367.6	54.0	526	10	AA416235 VF3B07.T
3	323.2	47.5	483	10	AA422330 VF45B09.T
4	246.6	36.2	557	10	BE110536 UI-R-BJ1-
5	237.4	34.9	462	13	AO729142 HS-5467-B
6	168	24.5	432	10	AA488294 UI-M-BH3-
7	167	24.5	443	10	AA500912 VG03404.T
8	148.2	21.8	377	11	BG203142 RST22516
9	138	20.3	370	11	BG197958 RST17210
10	137.8	20.3	598	11	AO670712 HS-5449-A
11	135	19.8	508	11	BG210970 RST30524
12	134.2	19.7	560	13	AA427288 CITR1-E1-

c	13	134.23	19.7	572	13	AA0427239 CITR1-E1-
14	125	18.4	470	10	AL110256 DKFZ6761J	
15	125	18.4	669	10	AL133928 DKFZ6761J	
c	16	119.6	17.6	589	13	AZ412330 1M0185C13
17	99	14.5	446	10	AA417843 ZV01C02.T	
c	18	91.4	13.4	470	13	AZ412322 1M0185A15
c	19	88.4	13.0	453	13	AO791237 HS_5495-A
c	20	86.8	12.7	366	10	AA446687 ZW84B08.T
c	21	83	12.2	794	10	AV700252 AV700252
22	76.4	11.2	194	10	AA149346 Z029C11.T	
23	75.4	11.1	424	11	BG359014 BOVMS1-02	
24	65.6	9.6	298	11	BF840611 MRL-HT106	
25	64.8	9.5	650	10	AA799431 EST188928	
c	26	64	9.4	377	10	AI399758 HS3A12.X
27	63.8	9.4	1245	12	AK006601 Mus muscu	
28	59.4	8.7	422	10	AA432886 VQ89C04.T	
29	59.4	8.7	450	11	BF543892 UI-R-BT0-	
30	59.2	8.7	525	11	BF077050 226844 MA	
31	57.4	8.4	826	11	BF344653 602015293	
32	57.4	8.4	876	11	BG682195 602629502	
33	56.4	8.3	772	10	AU123287 AU123287	
34	56.2	8.3	911	11	BG260067 602371653	
35	55.4	8.1	369	10	AA418446 56312 MAR	
36	55	8.1	419	10	AI106485 CB03C01.T	
37	54.8	8.0	868	11	BF670880 602149967	
38	54.4	8.0	809	10	AL520588 AL520588	
39	54.2	8.0	354	11	W75647 me49b12.r1	
40	54.2	8.0	400	10	AI385903 me49b12.Y	
41	54.2	8.0	567	10	BE664685 152497 MA	
42	53.2	7.8	586	10	AA662786 SWYD25CAU	
43	52.8	7.8	510	10	AW918885 EST350189	
44	52.8	7.8	613	10	AA441056 LD15830.5	
45	52.6	7.7	317	10	AA483293 52416 MAR	

ALIGNMENTS

RESULT 1	AK010252	LOCUS	AK010252	1450 bp	mus musculus ES cells cDNA, RIKEN full-length enriched library, clone:2400002D05, full insert sequence.	HTC	05-JUL-2001
ACCESSION	AK010252	VERSION	AK010252.1	GI:12845555			
KEYWORDS		SOURCE	AK010252.1	GI:12845555			
ORGANISM							
REFERENCE							
AUTHORS							
TITLE							
JOURNAL							
MEDLINE							
PUBMED							
REFERENCE							
AUTHORS							
1	(bases 1 to 1450)						
2	(bases 1 to 1450)						
3	(bases 1 to 1450)						
4	(bases 1 to 1450)						
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6	(bases 1 to 1450)						
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8	(bases 1 to 1450)						
9	(bases 1 to 1450)						
10	(bases 1 to 1450)						
11	(bases 1 to 1450)						
12	(bases 1 to 1450)						
13	(bases 1 to 1450)						
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31	(bases 1 to 1450)						
32	(bases 1 to 1450)						
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40	(bases 1 to 1450)						
41	(bases 1 to 1450)						
42	(bases 1 to 1450)						
43	(bases 1 to 1450)						
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45	(bases 1 to 1450)						

Query Match	72.5%;	Score 493.8;	DB 12;	Length 1450
Best Local Similarity	82.8%;	Pred. No. 1.7e-122;		

COMMENT Contact: Marra M/Mouse EST Project

QY	205	aagcaagcttaccattgttagatatactcagcaacaagtttccagtgctcccaatctgtctc	264
Db	120	AAGCAAGCTTACATTGTGGATATCTCTGGCAACAAGTTCTCCAGCGTTCTTATCTGTGTCT	179
QY	265	ctcgcgaatgtcgaatttgcagtggttgatatacagcaagaataacctgcacgcctgcgc	324
Db	180	CTCGGGAGTGTCTGTCTGTGAGTGGCTGTGATATCAGACAGAACAACTGTGATGACCTGGCA	239
QY	325	caaatatagacagagctagagagagctgcagagcttctcttctgtataaaacaagttgacc	384
Db	240	CAAAATATAGACAGAGCTGAGAGAGCTACAAAGTTTCTCTGTATATAAAACAAGCTGAC	299
QY	385	taccctccattatccatgcgcgaacccgaaagaaactcactctgtagctcagtgaggac	444
Db	300	TACCTTCCTCAAGCCATGCTCAACCTCAAAAAGCTCACTGCTGTGTCTCAGTGGGAGT	359
QY	445	catttgatgagagctcccaactgcctcttgtgtactatccacaccttaaatitgtgaac	504
Db	360	CACCTGTGGAGGTCGCCGACCGCCCTCTGTGGAAGCCCTCCACCGCTTGTGAATTTGTAGC	419
QY	505	ctatggacaatccattatgataatgtcccaatgtgtaagatgagcaatgaataatggaagt	564
Db	420	CTTGTGNCATTCCTCATTTGATTAAGACCGGATGTCAAGACATGAGACACATTAAGAGAC	479
QY	565	gaac	568
Db	480	GAGC	483
RESULT	4		
LOCUS	BE110536/c		
DEFINITION	BE110536	557 bp	mRNA
ACCESSION	U1-R-BJ1-ave-b-09-0-01.s1	U1-R-BJ1	Rattus norvegicus CDNA clone
VERSION	BE110536		
KEYWORDS	BE110536.1	GI:8502641	
SOURCE	EST.		
ORGANISM	Norway rat.		
	Rattus norvegicus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;		
	Rattus.		
REFERENCE	1 (bases 1 to 557)		
AUTHORS	Bonaldo,M.F., Lennon,G. and Soares,M.B.		
TITLE	Normalization and subtraction: two approaches to facilitate gene		
	discovery		
JOURNAL	Genome Res.	6 (9),	791-806 (1996)
MEDLINE	97044477		
COMMENT	Contact: Soares, MB		
	Program for Rat Gene Discovery and Mapping		
	University of Iowa		
	451 Eckstein Medical Research Building Iowa City, IA 52242, USA		
	Tel: 319 335 8250		
	Fax: 319 335 9565		
	Email: msquares@blue.weeg.uiowa.edu		
	The sequence contained an oligo-dT track that was present in the		
	oligonucleotide that was used to prime the synthesis of first		
	strand cDNA and therefore this may represent a bonafide poly A		
	tail. The sequence tag present in the cDNA between the NotI site		
	and the oligo-dT track served to identify it as a clone from the		
	normalized heart library cDNA Library Preparation: M.B. Soares Lab		
	Clone distribution: clones will be available through Research		
	Genetics (www.resgen.com)		
	Seq primer: M13 forward		
	PolyA=Yes.		
FEATURES			
Source	Location/Qualifiers		
	1..557		
	/organism="Rattus norvegicus"		
	/strain="Sprague-Dawley"		
	/db_xref="taxon:10116"		
	/clone="U1-R-BJ1-ave-b-09-0-01"		
	/clone_1lb="U1-R-BJ1"		

BASE COUNT	136 a	104 c	139 g	177 t	1 others
ORIGIN	TAG_SEQ=ACACAC"				
ORIGIN	TAG_TISSUE=heart				
ORIGIN	TAG_LIB=UI-R-BJ1				
ORIGIN	6:791-806, 1996)				
ORIGIN	described in (Bonaldo, Lennon and Soares, Genome Research				
ORIGIN	ratstc.eng.uiowa.edu. The subtraction has been previously				
ORIGIN	clone was derived, please visit our web site at				
ORIGIN	For a detailed description of the library from which this				
ORIGIN	AV canal at 15 dpc, ventricle at 13 dpc, and adult heart.				
ORIGIN	AV canal at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc,				
ORIGIN	tissues: atrium at 16.5 dpc, ventricle at 16.5 dpc, AV				
ORIGIN	Library is a subtracted library derived from the following				
ORIGIN	polylinker. Site_1: Not I; Site_2: Eco RI; The UI-R-BJ1				
ORIGIN	/lab.host="DB10B (Life Technologies)"				
ORIGIN	Note="vector: pUT3D-Pac (Pharmacia)" with a modified				
ORIGIN	Query Match				
ORIGIN	Best Local Similarity 36.2%; Score 246.6; DB 10; Length 557;				
ORIGIN	Matches 296; Conservative 0; Mismatches 65; Indels 1; Gaps 1;				
QY	320	tgccccaagata	taacacagcgtacagagctgcagagcttcctctctgtataaaacaagt	379	
DB	557	tgccccaagat	ttatcacagcgtgaaagcttaca	agtttcctcctgtatataaaacaagc	499
QY	380	tgacctacccttcctattccatctgctgaacctgaagaagctcaactctgttagtcgaagt	439		
DB	498	tgacctacccttcctgaacccatgcctcaacacctcaacacacccctgcgtgcttgcacagt	439		
QY	440	gggaccatttgtagagctcccaactgcctcttgtagctcaacacactttaaattg	499		
DB	438	gggagacctgtgtgagctcccgaccgccccttmtgcagtccttccacagccttggaaatttg	379		
QY	500	taagccttatgacacatcctattgataatgcccacatgtaagaatgacatgaataatg	559		
DB	378	taagcctttttggacacatcccatgtgacaaagcccatgtgcagacactgacacacagtag	319		
QY	560	aaagtgaacgggattgcgaacattttgataaagaagtatatgaagcctataatgaagcc	619		
DB	318	aaagcgaacagcagccgacgaccttgcgattgaaggaatttatgaamaacatcatcgaaagcc	259		
QY	620	ttaagaagaagaacatctgtccagcattatccacacaaagtgtctttgaccttaactt	679		
DB	258	tttaaggaaggaagacacgtcttccagcttattaccgccaagtgatcatgttagccttcaactt	199		
QY	680	ga	681		
DB	198	GA	197		
RESULT	5				
LOCUS	A0729142	462 bp	DNA	GSS	15-JUL-1999
DEFINITION	HS_5467_B2_B10_SP6E_RPCR-11 Human Male BAC Library Homo sapiens				
ACCESSION	A0729142				
VERSION	A0729142.1	GI:5500694			
KEYWORDS	GSS.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
TITLE	1 (bases 1 to 462)				
JOURNAL	Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D., and				
MEDLINE	Hood,L.				
COMMENT	Sequence-tagged connectors: A sequence approach to mapping and				
COMMENT	scanning the human genome				
COMMENT	Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)				
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L				

TITLE
The WashU-HHMI Mouse EST Project
JOURNAL
Unpublished (1996)
COMMENT
Contact: Marra M/Mouse EST Project

REFERENCE
AUTHORS
Marr,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubouque,T.
1 (bases 1 to 442)
Meir,A., Kneba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Geisel,S., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Thieling,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.

Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LINL; contact the
IMAGS Consortium (info@image.llnl.gov) for further information.
GRI:504351
putative full length read
vector to vector length is from Amersham
Seq primer: -28m13 rev2 ET from
high quality sequence stop: 362.

FEATURES
SOURCE

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/organism="Mus musculus"  
/strain="C57BL/6J"  
/db_xref="taxon:10090"  
/clone_image="860263"  
/clone_lib="Scars mouse NbMH"  
/sex="male"  
/tissue_type="heart"  
/dev_stage="4 weeks"  
/_lab_host="DH10B"  
/note=Vector:pT73D-Pac (Pharmacia) with a modified  
polylinker; Site_1: Not I; site_2: Eco RI; 1st strand  
cDNA:TCGATCGATGTGAAGGGGACGCCGCGAAGTTTTTTTTTTTTTTTTTTT  
3'; double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not  
I and Eco RI sites of the modified pT73 vector. RNA  
provided by Dr. Minoru Ko, Wayne State Univ. Library  
constructed and normalized by Bento Soares and M.Fatima  
Conaldi."
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BASE COUNT	133 a	94 c	94 g	122 t
ORIGIN				
Query Match		24.5%;	Score 167;	DB 10; Length 443;
Best Local Similarity		80.8%;	Pred. No. 1.5e-34;	
Matches 219; Conservative		0;	Mismatches 50;	Indels 2; Gaps 2;
QY 413 agaagctacctctgtttatctgltcaglygggagccatttgytga-gctccaaactgcccctt 471				
Db 1 AAAACCTCACCTCTGGTGGTGTGCATGTGGGAGACCTGTGTGACGCTCCGACCCGCCCTTC 60				
QY 472 ttgtgcatcatcacaccccttaaatcttgaagccctatggagacatccctatgataatgcc 531				
Db 61 TGGCATGECCTCCACGCCCTTTGAATTTGTGAAGCCTTTGGACAATCCATTATATGAAGCC 120				
QY 532 caatltgaaagatlygccaatgaaataatggaagaatggaacggaatcgcgaac-atttgatga 590				
Db 121 GGAATGTCAAGACACTGAAGACACACAGTAGAGAGCGAGCGGACCGCAGGATTTTGATGA 180				
QY 551 agaagatgaaagccctatattgaagacccttaagaagaagaatctgttccagctatac 650				
Db 181 GGAATTTTGAAGAAGCATTTATTTGAAGACCTTAAAGAAAGAGAAAGACTGTTCACGATTATAC 240				
QY 651 caccaaagtgtctttagccttcaacttga 681				
Db 241 GACCAAGGTGTCAATTTAGTCTTCACCTTGA 271				

[illegible]

REFERENCE AUTHORS	TITLE	JOURNAL	COMMENT
1 (pages 1 to 377) Harrington J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Dall, T., Thornton, M., Ramachandran, R., Whittington, J., Tierne, L., Krashoc, D., McElligott, K., Clark, S., Mays, R., Smith, E., Veloso, N., Hess, J.G., Colhoun, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.	Creation of Genome-wide Protein Expression Libraries using Random		
	Activation of Gene Expression		
	Nat. Biotechnol. 19 (5), 440 (2001)	In press	
Contact: Scott J. Cain			

Activation of Gene Expression
Nat. Biotechnol. 19 (5), 440 (2001) In press
Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave., Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 377.

FEATURES
source

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
BASE COUNT      139 a      66 c      65 g      104 t
ORIGIN

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Query Match	21.88; Score 148.2; DB 11; Length 377;
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RESULT 11
LOCUS BG210970 508 bp mRNA EST 21-APR-2001
DEFINITION RST30524 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG210970
VERSION BG210970.1 GI:13732657
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 508)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
Cain,S., Dahl,T., Thornton,M., Ramachandran,R., Whittington,J.,
Lerner,L., Krashoc,D., McElligott,K., Clark,S., Mays,R., Smith,E.,
Velasco,N., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J.
and Ducar,M.
TITLE Creation of genome-wide Protein Expression Libraries using Random
Activation of Gene Expression
JOURNAL Nat. Biotechnol. 19 (5), 440 (2001) In press
COMMENT Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scai@atersys.com
High quality sequence stop: 508.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Athersys RAGE Library"
/cell_line="HT1080"
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
BASE COUNT 182 a 81 c 83 g 160 t
ORIGIN
Query Match 19.8%; Score 135; DB 11; Length 508;
Best Local Similarity 98.1%; Pred. No. 6.5e-26;
Matches 157; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
OY 522 tgataatcccaatgtgaagatggaatgaataatgaagaatggaacggaatcgcaaca 581
DB 33 TGNRAATCCCAATGTG-AGATGGCAATGAAT-ATGGAAGTGAACGGGATCGCCACA 90
OY 582 ttctgataaagaagttatgaagcctatatgaagacctaagaagaagaatctgttc 641
DB 91 TTTTGATTAAGAGTTATGAAGACCTATATGAAGACCTTAAGAAGAAGATCTGTCC 150
OY 642 cagctataccaccaaagtgtcttttaagcctcaacttga 681
DB 151 CAGCTATACACCAAGTGTCTTTTAAAGCTTCAACTTTGA 190
RESULT 12
LOCUS AQ427288/c 560 bp DNA GSS 24-MAR-1999
DEFINITION CITBI-EI-2568D1.TR CITBI-EI Homo sapiens genomic clone 2568D1, DNA
sequence.
ACCESSION AQ427288
VERSION AQ427288.1 GI:4500038
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 560)

AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venier,J.C.
TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Other-GSSs: CITBI-EI-2568D1.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hoe@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES
1..560
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2568D1"
/clone_lib="CITBI-EI"
/sex="male"
/cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
Caltech Human BAC Library D"
BASE COUNT 132 a 154 c 101 g 173 t
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Best Local Similarity 91.6%; Pred. No. 1.1e-25;
Matches 153; Conservative 0; Mismatches 13; Indels 1; Gaps 1;
OY 1 atgaagaatctggatctgcccaaaaacaaatctacatcttcgcagagaatcggtgt 60
DB 167 ATGAGAAATTCAGGATCTGCCAAGAACAAATCTCCATTTTCCAGCTAACTCAGTTGT 108
OY 61 ttgaagaacctgaagaagactcaatgtgggttcaactatctgaagaagcattccctcagaa 120
DB 107 TTGAAGACCTGAATTAATCAATGTGATTTCAACTCTGGAAGAGCATTCCTCCAGAG 48
OY 121 ttggagatctggaatctagagagactgtagtcttggaatct 167
DB 47 CTGGGAGATTGTG-AAATCTAGAGGAGGACTGATTGTCTGGAATCT 2
RESULT 13
LOCUS AQ427239/c 572 bp DNA GSS 24-MAR-1999
DEFINITION CITBI-EI-2568B9.TR CITBI-EI Homo sapiens genomic clone 2568B9, DNA
sequence.
ACCESSION AQ427239
VERSION AQ427239.1 GI:4499942
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 572)
AUTHORS Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venier,J.C.
TITLE Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
Map Building
JOURNAL Unpublished (1997)
COMMENT Other-GSSs: CITBI-EI-2568B9.TF
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200

Fax: 301 838 0208
 Email: hbe@ligr.org
 Clones are available from Research Genetics (info@resgen.com). BAC
 end search page: http://www.ligr.org/tdb/humgen/bac_end_search/bac_end_search.html.
 Seq primer: M13 Reverse
 Class: BAC ends.

FEATURES

Location/Qualifiers
 1..572

source
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="2568B9"
 /clone_lib="CITBI-EI"
 /sex="male"
 /cell_type="sperm"
 /note="Vector: pBelOBAcl1; Site_1: EcoRI; Site_2: EcoRI;
 Caltech Human BAC library D"
 BASE COUNT 134 a 157 c 104 g 177 t
 ORIGIN

Query Match 19.7%; Score 134.2; DB 13; Length 572;
 Best Local Similarity 91.6%; Pred. No. 1.1e-25;
 Matches 153; Conservative 0; Mismatches 13; Indels 1; Gaps 1;

OY 1 atggaattctgattctgcacaaaccacatctcacatcttcacagcagaatcgattgt 60
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 167 ATGGAATTCAGATCGATCGCAACAAACAATCTCACATTTTCCAGCTAAACTAGTTGT 108
 OY 61 ttgaagaacctgaagaactcaatctgtgttcaactatctgaagaacatctccacga 120
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 107 TTGAAGAACCCTGAATATACATCATGTGAGTTTCAACTATCTGAAGAGATTCCTCCAGAG 48
 OY 121 ttgggaattgtgaaatctagagaactgattgttcttgaactct 167
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 47 CTGGGAGATTGTG-AAATCTAGAGGACTGATTGTTCTGGAAATCT 2

RESULT 14

AL120256 470 bp mRNA EST 25-FEB-2000
 LOCUS DKFZP761J017_x1 761 (synonym: hamy2) Homo sapiens cDNA clone
 DEFINITION DKFZP761J017 5', mRNA sequence.
 ACCESSION AL120256
 VERSION AL120256.1 GI:5926155
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 JOURNAL 1 (bases 1 to 470)
 COMMENT Koehler K., Beyer A., Mewes H.W., Gassenhuber J. and Wiemann S.
 EST (Koehler, et al.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Koehler K

MIPS
 Am Klopferpitz 18a D-82152 Martinsried, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by BMFZ (Biomedical Research Center at the Charite,
 Berlin/Germany) within the cDNA sequencing consortium of the German
 Genome Project.
 No sl sequence available.

This clone (DKFZP761J017) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source

1..470
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="DKFZP761J017"
 /clone_lib="761 (synonym: hamy2)"

/tissue_type="amygdala"
 /dev_stage="adult"
 /lab_host="DH108"
 /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"
 BASE COUNT 166 a 73 c 77 g 150 t 4 others
 ORIGIN

Query Match 18.4%; Score 125; DB 10; Length 470;
 Best Local Similarity 100.0%; Pred. No. 3.1e-23;
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 557 tggaaagtgaacggatcgccacatttgaataaagaattgaagcctatataga 616
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 1 TGGAAAGGAGACGGGATCGCCACATTTTGATTAAGAAGTATGAAACCTATATGAG 60
 OY 617 acctaaagaagaagaatctgttccagctatcacaccagaatgcttttagcttcaac 676
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
 Db 61 ACCTTAAGAAGAAGAAATCTGTCCACCTATACACCAAGTGTCTTTAGCCTTCAC 120
 OY 677 ttga 681
 |||||||
 Db 121 TTGA 125

RESULT 15

AL133928 669 bp mRNA EST 25-FEB-2000
 LOCUS DKFZP761O1814_x1 761 (synonym: hamy2) Homo sapiens cDNA clone
 DEFINITION DKFZP761O1814 5', mRNA sequence.
 ACCESSION AL133928
 VERSION AL133928.1 GI:6602115
 KEYWORDS EST.
 SOURCE human.

REFERENCE
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 JOURNAL 1 (bases 1 to 669)
 COMMENT Ansoerge W., Winkner U., Mewes H.W., Well B. and Wiemann S.
 EST (Ansoerge, W., Winkner, U., Mewes, H.W., Well, B. and Wiemann, S.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Ansoerge W

MIPS
 Am Klopferpitz 18a D-82152 Martinsried, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 sequenced by EMBL (European Molecular Biology Laboratories,
 Heidelberg/Germany) within the cDNA sequencing consortium of the
 German Genome Project.
 No sl sequence available.

This clone (DKFZP761O1814) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source
 1..669

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="DKFZP761O1814"
 /clone_lib="761 (synonym: hamy2)"
 /tissue_type="amygdala"
 /dev_stage="adult"
 /lab_host="DH108"
 /note="Vector: pSport1; Site_1: NotI; Site_2: SalI"

BASE COUNT 214 a 118 c 141 g 196 t
 ORIGIN

Query Match 18.4%; Score 125; DB 10; Length 669;
 Best Local Similarity 100.0%; Pred. No. 3.4e-23;
 Matches 125; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 557 tggaaagtgaacggatcgccacatttgaataaagaattgaagcctatataga 616

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Db      1  TGAAGTGAACGGGATGCCACATTTGATAAAGAGTTATGAAGCTATATTGAAG 60
OY      617  acctaaagaagaagaaatcgttcccaagctataccaccaagtgctctttagccctcaac 676
Db      61  ACCTTAAGAAGAAGAAATCTGTCCAGCTATACCACCAAGTGTCTTTAGCCTTCAAC 120
OY      677  tttaga 681
Db      121  TTTGA 125
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Job time: 16316 sec